Figure 1

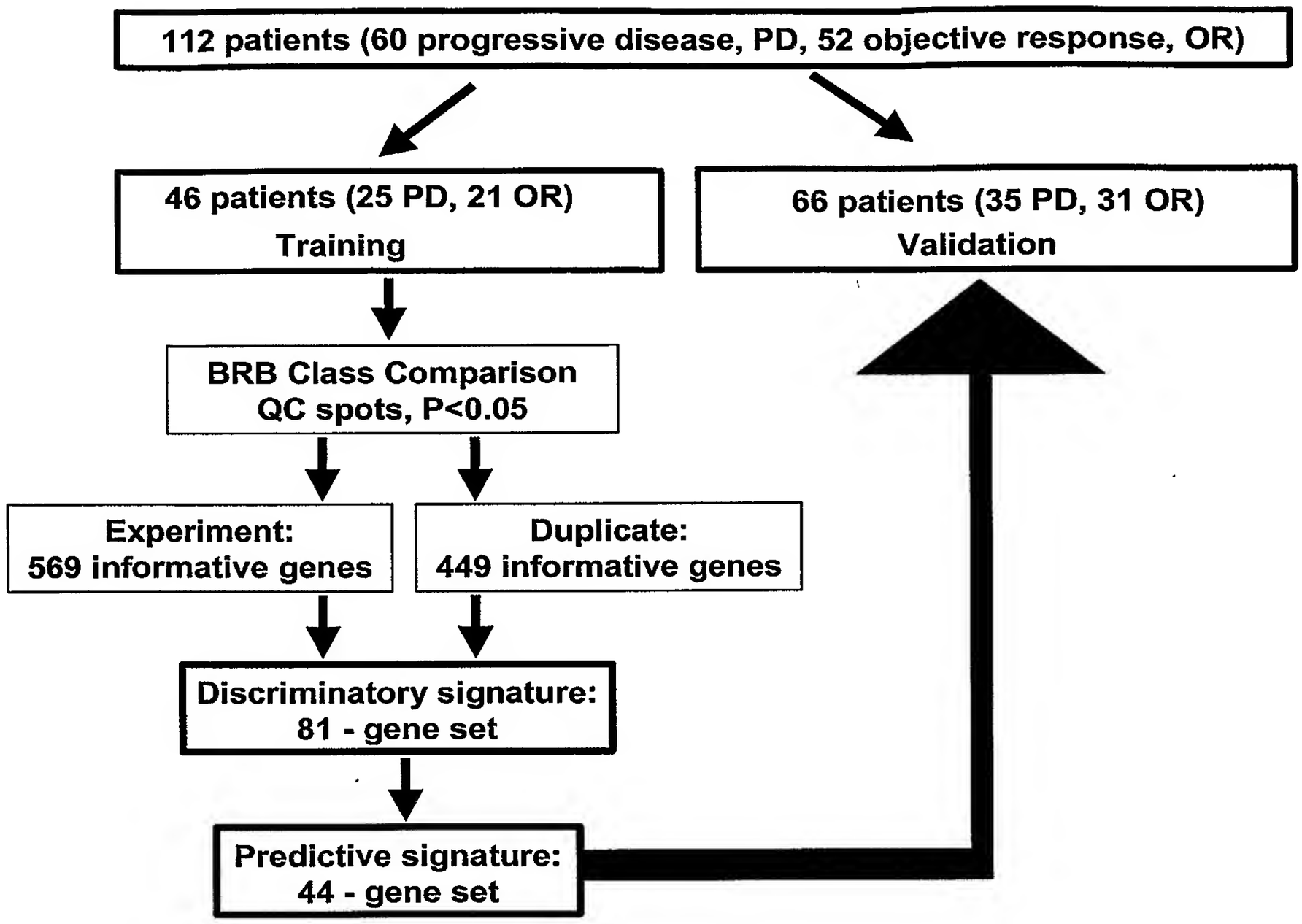
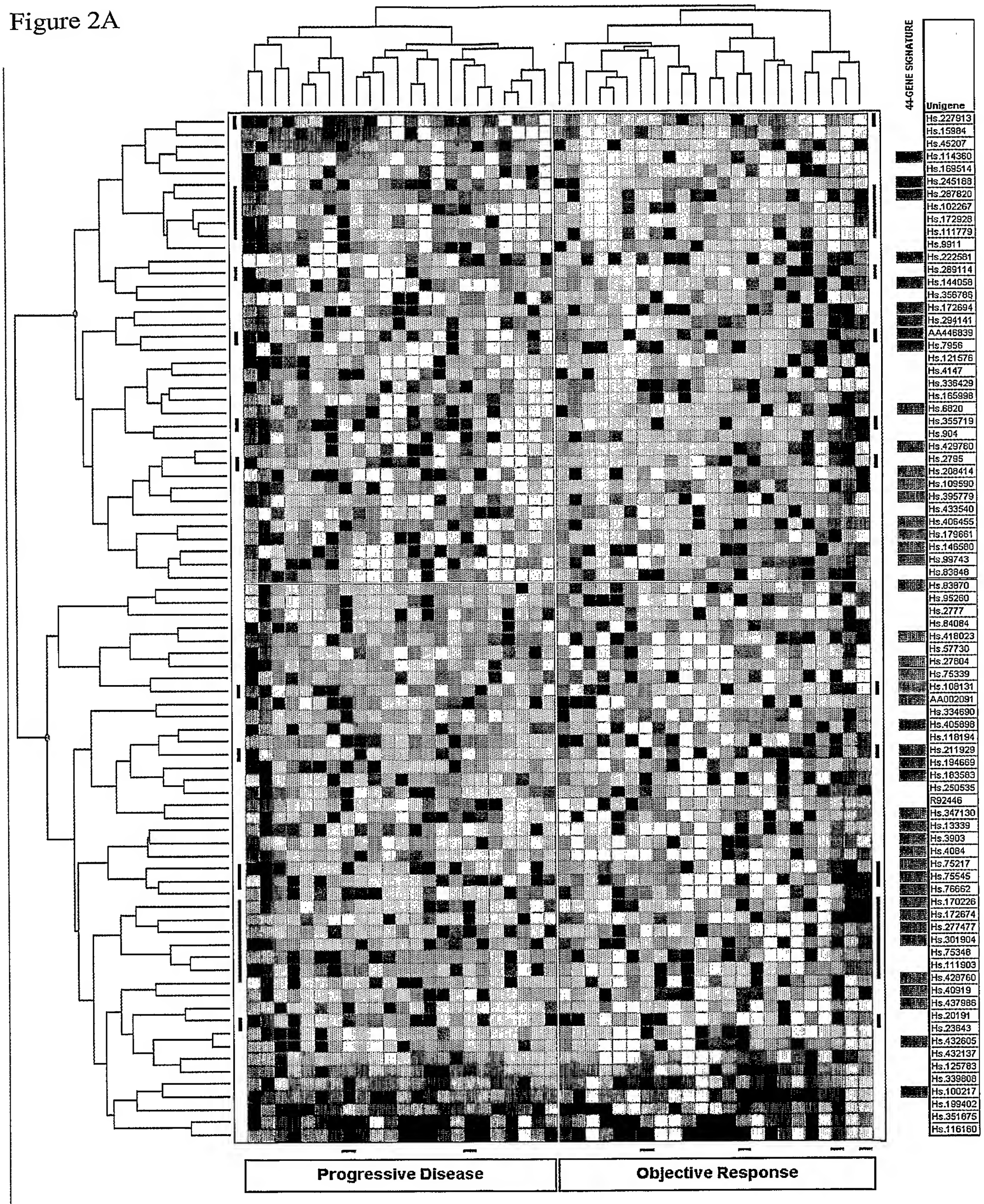

112 patients (60 progressive disease, PD, 52 objective response, OR)
46 patients (25 PD, 21 OR)
Training
66 patients (35 PD, 31 OR)
Validation
BRB Class Comparison
QC spots, P<0.05
Experiment:
569 informative genes
Duplicate:
449 informative genes
Discriminatory signature:
81 - gene set
Predictive signature:
44 - gene set

Figure 2A



Cluster I Cluster II

Figure 2B

44-GENE SIGNATURE	Unigene	Gene_Symbol	Location	SWISSPROT Keywords	ER regulation
	Hs.227913	API5	11p12-q12		
	Hs.15984	LOC51186	Xq22.1		8
	Hs.45207	CHD6-pending	20q12		
	Hs.114360	TSC22	13q14	Transcription regulation; Repressor; Nuclear protein.	21
	Hs.169514				
	Hs.245188	TIMP3	22q12.3	Metalloprotease inhibitor.	19
	Hs.287820	FN1	2q34	Cell adhesion.	
	Hs.102267	LOX	5q23.2		
	Hs.172928	COL1A1	17q21.3-q22.1	Extracellular matrix.	
	Hs.111779	SPARC	5q31.3-q32	Extracellular matrix.	17
	Hs.9911	FLJ11773	12q13.13		
	Hs.222581				
	Hs.289114	TNC	9q33	Extracellular matrix; Cell adhesion.	
	Hs.144058	DKFZP564C103	17q25.2		
	Hs.356786	GNAQ	9q21.2		
	Hs.172694	LOC117584	17q12		
	Hs.294141	SMARCA4	19p13.3		
	AA446839	BNIP3	10q26.3		
	Hs.7956				
	Hs.121576	MYO1B	2q12-q34	Myosin; ATP-binding; Actin-binding; Calmodulin-binding.	
	Hs.4147	TRAM	8q13.1	Endoplasmic reticulum; Transmembrane; Glycoprotein.	
	Hs.336429	GABARAPL1	12p13.31		17
	Hs.165998	PAI-RBP1	1p31-p22		
	Hs.6820	CFP1	10p11.21		8
	Hs.355719	NPM1	5q35	Nuclear protein; Phosphorylation; RNA-binding; Proto-oncogene.	
	Hs.904	AGL	1p21	Glycogen biosynthesis; Glycosyltransferase.	
	Hs.429780				
	Hs.2795	LDHA	11p15.4	Oxidoreductase; NAD; Glycolysis.	20
	Hs.208414				
	Hs.109590	GENX-3414	4q24-q25		
	Hs.395779	CAMTA1	1p36.23		
	Hs.433540	DNAJC8	1p35.2	Chaperone.	
	Hs.406455	PSAP	10q21-q22	Glycoprotein; Lysosome; Sphingolipid metabolism.	
	Hs.179661	OK/SW-cl.56	6p21.33	Microtubule; GTP-binding.	
	Hs.146560	ENO2	12p13	Lyase; Glycolysis; Magnesium.	17
	Hs.99743				18
	Hs.83848	TPI1	12p13	Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis.	
	Hs.83870	NEB	2q22	Actin-binding; Muscle protein; Cytoskeleton.	
	Hs.95260	FAM8A1	6p22-p23		
	Hs.2777	ITIH1	3p21.2-p21.1	Serine protease inhibitor.	
	Hs.84084	APPBP2	17q21-q23		
	Hs.418023				
	Hs.57730	KIAA0133	1q42.13	Hypothetical protein; Transmembrane.	
	Hs.27804				
	Hs.75339	INPPL1	11q23		
	Hs.108131	CASP2	7q34-q35	Hydrolase; Thiol protease; Apoptosis.	
	AA002091	CACH-1	5q14.1		
	Hs.334690				
	Hs.405898	KIAA0999	11q23.3		
	Hs.118194	DBR1	3q22.3		
	Hs.211929	TXN2	22q13.1	Redox-active center; Electron transport; Mitochondrion.	8
	Hs.194669	EZH1	17q21.1-q21.3	Transcription regulation; Nuclear protein; DNA-binding.	
	Hs.183583	SERPINB1	6p25	Serpin; Serine protease inhibitor.	
	Hs.250535	RAB5EP	17p13.2		
	R92446				
	Hs.347130	FLJ22709	19p13.11		
	Hs.13339	PRPSAP2	17p11.2-p12		
	Hs.3903	CDC42EP4	17q24-q25	Cytoskeleton.	21
	Hs.4084	KIAA1025	12q24.22		
	Hs.75217	MAP2K4	17p11.2	Serine/threonine-protein kinase; Tyrosine-protein kinase.	
	Hs.75545	IL4R	16p11.2-12.1	Receptor; Transmembrane; Glycoprotein.	
	Hs.76662	APH2	10q24.1		
	Hs.170226	FLJ38045	9q33.1		
	Hs.172674	NFATC3	16q22.2	Transcription regulation; Activator; Nuclear protein; DNA-binding.	
	Hs.277477	HLA-C	6p21.3	MHC I; Transmembrane; Glycoprotein.	18
	Hs.301904	FLJ12671	1q21.3		
	Hs.75348	PSME1	14q11.2	Proteasome; Interferon induction.	8
	Hs.111903	FCGRT	19q13.3	IgG-binding protein; Receptor; Transmembrane; Glycoprotein.	
	Hs.428760				
	Hs.40919	FLJ14511	9q22.33		
	Hs.437986				8
	Hs.20191	SIAH2	3q25		8
	Hs.23643	MST4	Xq26.1		
	Hs.432605	UGCG	9q31	Glycosyltransferase; Endoplasmic reticulum.	17
	Hs.432137	DLX2			
	Hs.125783	DEME-6	1p32.3		
	Hs.339808	KIAA0563	17q21.31		
	Hs.100217	FMNL	17q21		8
	Hs.199402	UFD1L	22q11.21	Ubl conjugation pathway.	
	Hs.351875	COX6C	8q22-q23	Oxidoreductase; Inner membrane; Mitochondrion.	
	Hs.116160				

Figure 3

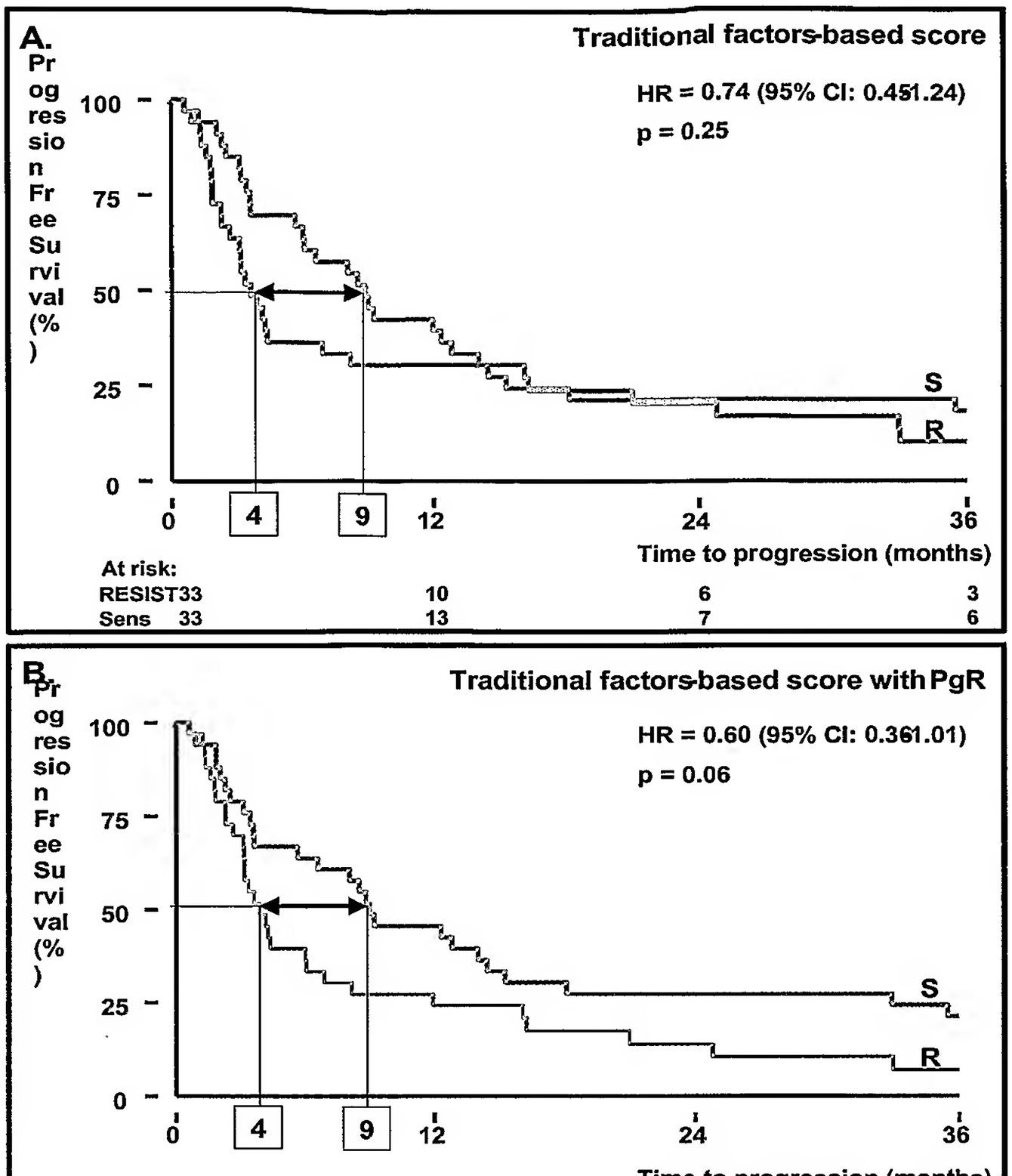
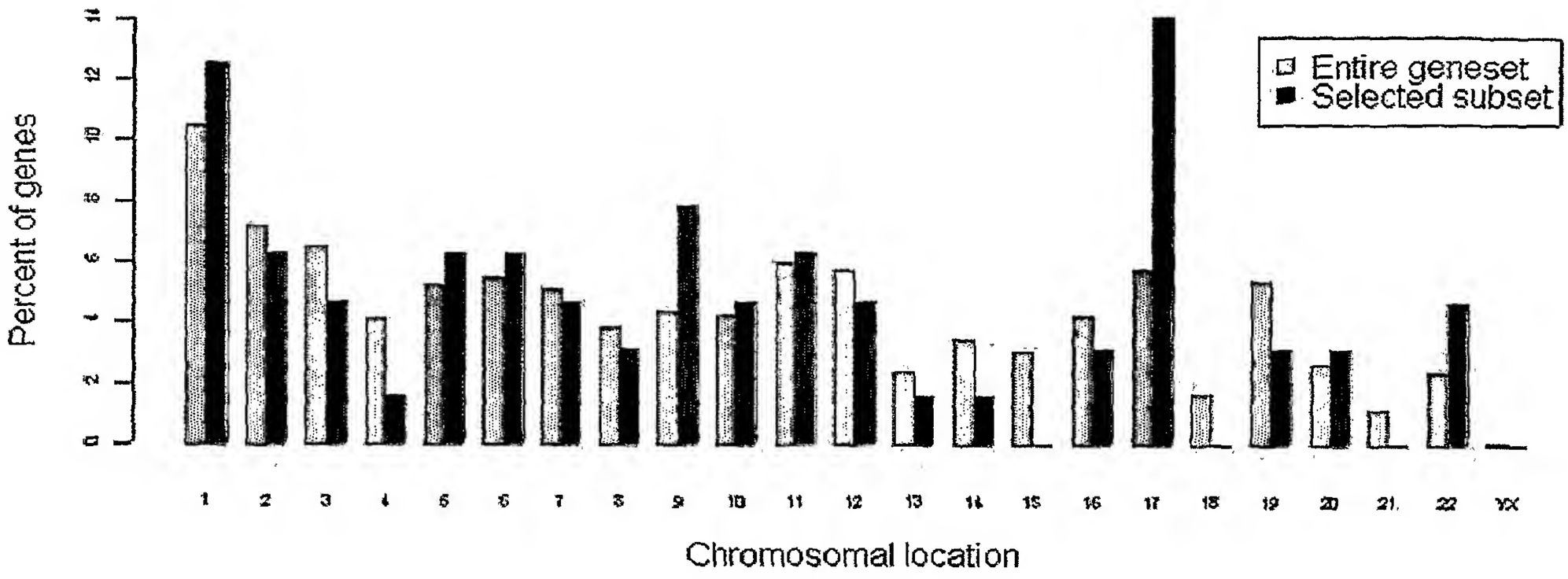

A.
Traditional factors-based score
HR = 0.74 (95% CI: 0.451.24)
p = 0.25
Progression Free Survival (%)
100
75
50
25
0
S
R
0
4
9
12
24
36
Time to progression (months)
At risk:
RESIST33 10 6 3
Sens 33 13 7 6
B.
Traditional factors-based score with PgR
HR = 0.60 (95% CI: 0.361.01)
p = 0.06
Progression Free Survival (%)
100
75
50
25
0
S
R
0
4
9
12
24
36
Time to progression (months)
At risk:
Resist 33 8 4 2
sens 33 15 9 7
C.
44-gene signature based classification
HR = 0.54 (95% CI: 0.310.94)
p = 0.03
Progression Free Survival (%)
100
75
50
25
0
S
R
0
4
12
15
24
36
Time to progression (months)
At risk:
RESIST43 10 4 3
sens 23 13 9 6

Figure 4


Entire geneset
Selected subset
Percent of genes
0
2
4
6
8
10
12
14
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
XX
Chromosomal location